(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GCCGGCCATG GCCARKGCTG GDGTCACTC 29

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GCCGGCCATG GCCAATGCCG GCGTCATGC 29

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GCCGGCCATG GCCGRTRCTG GAGTCTCCC 29

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GCCGGCCATG GCCGATGCTR GARTCACCC 29

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GCCGGCCATG GCCGATTCTG GAGTCACAC 29

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GCCGGCCATG GCCGAYGCTG GWGTTATCC 29

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GCCGGCCATG GCCGATGCTG RYRTTAYCC 29

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GCCGGCCATG GCCGAAGCTG GAGTTACTCA G 31

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GCCGGCCATG GCCGATGCTA CTATTCATCA ATGGCC 36

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GCTGCCACCG CCACCCACCT TGTTCAGGTC C 31

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GCTGCCACCG CCACCCACGT TTTCAGGTCC 30

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GGAGGCGGCG GTTCTGCTAA GAGACCACMC AGCC 34

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GGAGGCGGCG GTTCTCAGAA GRTAACTCAA RCSC 34

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GGAGGCGGCG GTTCTCAGTC KGTGASCCAG C 31

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GGAGGCGGCG GTTCTCAGAG AGTGACTCA GCC 33

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GGAGGCGGCG GTTCTCWGMA SGTGRAACAA RGTCC 35

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GGAGGCGGCG GTTCTCAGCA AGTTAAGCAA AATTC 35

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GGAGGCGGCG GTTCTGAGAR TGTGGRGCWG CATC 34

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GGAGGCGGCG GTTCTAAKGA RGTGGMGCAG RRTYC 35

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GGAGGCGGCG GTTCTCAGCT GCTGGAGCAG AG 32

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GGAGGCGGCG GTTCTCAAMA GRKAGAASAG RATYC 35

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GGAGGCGGCG GTTCTGGACA AARCMTTGAR CAG 33

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GGAGGCGGCG GTTCTAAGGA CCAAGTGTTT CAG 33

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

TTCATAGACT AGTAGGGTCA GGGTTCTGG 29

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GGTGGCGGTG GCAGCGGCGG TGGTGGTTCC GGAGGCGGCG GTTCT 45

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CCACCGCCAC CGTCGCCCGC CACCACCAAG GCCATCCGCC GCCAAGA 47

What is claimed is:

1. A soluble fusion protein comprising a bacteriophage coat protein covalently linked to a single-chain T cell receptor, wherein the single-chain T cell receptor comprises a V-α chain covalently linked to a V-β chain by a peptide linker sequence.

2. The soluble fusion protein of claim 1, wherein the C-terminus of the V-α chain is covalently linked by the peptide linker sequence to the N-terminus of V-β chain.

3. The soluble fusion protein of claim 1, wherein the C-terminus of the V-β chain is covalently linked by the peptide linker sequence to the N-terminus of the V-α chain.

4. The soluble fusion protein of claim 2 further comprising a C-β chain fragment covalently linked between the C-terminus of the V-β chain and the N-terminus of the bacteriophage coat protein.

5. The soluble fusion protein of claim 2 further comprising a C-α chain fragment covalently linked between the C-terminus of the V-α chain and the N-terminus of the peptide linker sequence.

6. The soluble fusion protein of claim 2, wherein the fusion protein further comprises at least one protein tag.

7. The soluble fusion protein of claim 2, wherein the peptide linker sequence contains from approximately 2 to 20 amino acids.

8. The soluble fusion protein of claim 1, wherein the bacteriophage coat protein is gene III or gene VIII protein.

9. A soluble fusion protein comprising covalently linked in sequence: 1) a V-α chain, 2) a peptide linker sequence, 3) a V-β chain and 3) a bacteriophage gene III protein.

10. The soluble fusion protein of claim 9 further comprising a C-β chain fragment covalently linked between the C-terminus of the V-β chain and the N-terminus of the bacteriophage gene III protein.

11. The soluble fusion protein of claim 10, further comprising a protein tag covalently linked to the C-terminus of the C-β fragment and the N-terminus of the bacteriophage gene III protein.

12. The soluble fusion protein of claim 9 further comprising a first protein tag covalently linked between the C-terminus of the V-β chain and

the N-terminus of the bacteriophage gene III protein, and a second protein tag covalently linked to the C-terminus of the fusion protein.

13. A soluble fusion protein comprising covalently linked in sequence: 1) a V-α chain, 2) a peptide linker sequence, 3) a V-β chain, and 4) a bacteriophage gene VIII protein.

14. A soluble fusion protein comprising covalently linked in sequence: 1) a V-α chain, 2) a peptide linker sequence, 3) a V-β chain covalently linked to a C-β chain fragment, and 4) a bacteriophage gene VIII protein.

15. A soluble fusion protein comprising covalently linked in sequence: 1) a V-α chain covalently linked to a C-α chain fragment, 2) a peptide linker sequence, 3) a V-β chain covalently linked to a C-β chain fragment, and 4) a bacteriophage gene VIII protein.

16. The soluble fusion protein of claim 13 further comprising a first protein tag covalently linked to the C-terminus of the V-β chain and the N-terminus of the gene VIII protein, and a second protein tag covalently linked to the C-terminus of the fusion protein.

17. The soluble fusion protein of claim 14 or 15 further comprising a protein tag covalently linked to the C-terminus of the C-β chain fragment and the N-terminus of the gene VIII protein.

18. The soluble fusion protein of claim 2, wherein the V-α and V-β chains are isolated from cytotoxic T cells.

19. A single-chain T cell receptor produced by cleaving the one or more protein tags from the soluble fusion protein of claim 6.

20. The single-chain T cell receptor of claim 19, wherein the single-chain T cell receptor has been humanized.

21. A DNA segment comprising a sequence encoding a soluble fusion protein, the soluble fusion protein comprising a bacteriophage coat protein covalently linked to a single-chain T cell receptor, wherein the DNA segment further comprises an operably linked promoter and linker sequence.

22. A DNA segment comprising a sequence encoding a soluble fusion protein comprising covalently linked in sequence: 1) a V-α chain, 2) a peptide linker sequence, 3) a V-β chain and 3) a bacteriophage gene III protein.

23. A DNA segment comprising a sequence encoding a soluble fusion protein comprising covalently linked in sequence: 1) a V-α chain, 2) a peptide linker sequence, 3) a V-β chain, and 4) a bacteriophage gene VIII protein.

24. A DNA segment comprising a sequence encoding a soluble fusion protein comprising covalently linked in sequence: 1) a V-α chain, 2) a peptide linker sequence, 3) a V-β chain covalently linked to a C-β chain fragment, and 4) a bacteriophage gene VIII protein.

25. A DNA segment comprising a sequence encoding a soluble fusion protein comprising covalently linked in sequence: 1) a V-α chain covalently linked to a C-α chain fragment, 2) a peptide linker sequence, 3) a V-β chain covalently linked to a C-β chain fragment, and 4) a bacteriophage gene VIII protein.

26. The DNA segment of claim 23 further comprising a sequence encoding a protein tag covalently linked between the 3' end of the sequence encoding the V-β chain and the 5' end of the sequence encoding the bacteriophage gene VIII protein.

27. The DNA segment of claim 24 or 25 further comprising a sequence encoding a protein tag covalently linked between the 3' end of the sequence encoding the C-β chain fragment and the 5' end of the sequence encoding the bacteriophage gene VIII protein.

28. The DNA segment of claim 26 further comprising sequence encoding a protein tag covalently linked to the 3' end of the sequence encoding the fusion protein.

29. A DNA vector comprising the DNA segment of claim 21.

30. The DNA segment of claim 21, wherein the promoter and linker are phoA and pelB from E. coli, respectively.

31. A bacteriophage library comprising bacteriophages displaying soluble fusion proteins, wherein each of the soluble fusion proteins comprises a bacteriophage coat protein covalently linked to a single-chain T cell receptor, wherein each single-chain T cell receptor comprises a V-α chain covalently linked to a V-β chain by a peptide linker sequence.

32. The bacteriophage library of claim 31, wherein the C-terminus of the V-α chain is covalently linked by the peptide linker sequence to the N-terminus of V-β chain.

33. The bacteriophage library of claim 31, wherein the C-terminus of the V-β chain is covalently linked by the peptide linker sequence to the N-terminus of the V-α chain.

34. The bacteriophage library of claim 31, wherein the soluble fusion protein further comprises at least one protein tag.

35. The bacteriophage library of claim 31, wherein the V-α and V-β chains are isolated from an immunologically naive mammal.

36. The bacteriophage library of claim 31, wherein the V-α and V-β chains are isolated from a mouse.

37. The bacteriophage library of claim 31, wherein the mouse includes a transgene capable of expressing an HLA-A2 antigen complex.

38. The bacteriophage library of claim 31, wherein the V-α and V-β chains are obtained from a human suffering from or suspected of having cancer, an infectious disease, an autoimmune disorder, or an allergy.

39. The bacteriophage library of claim 31, wherein the infectious disease is an infection by an RNA or DNA virus.

40. The bacteriophage library of claim 39, wherein the RNA virus is a human immunodeficiency virus.

41. The bacteriophage library of claim 39, wherein the DNA virus is selected from the group consisting of cytomegalovirus, adenovirus, polyoma virus, influenza, or pox virus.

42. The bacteriophage library of claim 31, wherein the bacteriophage coat protein is gene VIII protein.

43. A kit comprising the bacteriophage display library of claim 31, a host cell sample, and directions for using the kit.

44. A bacteriophage library comprising bacteriophages displaying soluble fusion protein muteins, wherein each of the soluble fusion protein muteins comprises a bacteriophage coat protein covalently linked to a single-chain T cell receptor mutein.

45. A method of isolating a soluble fusion protein comprising a bacteriophage coat protein covalently linked to a single-chain T cell receptor, the method comprising:

introducing into host cells a DNA vector comprising a sequence encoding the fusion protein,

culturing the host cells in cultured medium under slow induction conditions which permit expression of the fusion protein; and

purifying the fusion protein from the host cell or the medium to isolate the soluble fusion protein.

46. The method of claim 45, wherein the method further comprises contacting an extract of the host cell or the cultured medium with a synthetic matrix capable of specifically binding the fusion protein, and purifying the fusion protein from the synthetic matrix to isolate the soluble fusion protein.

47. A method of isolating a DNA segment comprising a sequence encoding a soluble fusion protein, the soluble fusion protein comprising a bacteriophage coat protein covalently linked to a single-chain T cell receptor, the method comprising:

infecting host cells with a bacteriophage library comprising bacteriophages displaying soluble fusion proteins, wherein each of the fusion proteins comprises the bacteriophage coat protein covalently linked to the single-chain T cell receptor,

culturing the host cells under slow induction conditions which permit propagation of the bacteriophages,

contacting the bacteriophages with a molecule under conditions which permit specific binding between the molecule and at least one of the bacteriophages to produce at least one bacteriophage comprising a specific binding complex,

identifying one of the bacteriophages comprising the specific binding complex,

propagating the bacteriophage; and

isolating the DNA segment from the bacteriophage.

48. The method of claim 47 further comprising inserting the DNA segment into a DNA vector capable of expressing the soluble fusion protein in the host cell.

49. A method of expressing a soluble single-chain T cell receptor, the method comprising:

introducing into host cells a DNA vector comprising a sequence encoding the soluble single-chain T cell receptor,

culturing the host cells in medium under conditions which permit expression of the soluble single-chain T cell receptor; and

purifying the single-chain T cell receptor from the host cell or the medium to isolate the soluble single-chain T cell receptor.

50. The method of claim 49, wherein the host cells are selected from the group consisting of bacterial, insect or mammalian cells.

51. A method of increasing the specific binding affinity of a single-chain T cell receptor for a ligand, the method comprising:

determining a first specific binding affinity between the single-chain T cell receptor and the ligand,

infecting host cells with the bacteriophage library of claim 44, the infecting being under conditions which permit propagation of the bacteriophages,

contacting the host cells with the ligand sufficient to permit specific binding between at least one of the bacteriophages and the ligand to produce at least one specific binding complex between the bacteriophage and the ligand,

identifying one of the bacteriophages comprising the specific binding complex,

isolating DNA from the bacteriophage, the DNA comprising a sequence encoding a soluble fusion protein mutein and expressing the soluble fusion protein mutein,

separating a soluble single-chain T cell receptor mutein from the soluble fusion protein mutein,

determining a second specific binding affinity between the single-chain T cell receptor mutein and the ligand; and

identifying the single-chain T cell receptor with increased specific binding affinity for the ligand as the single-chain T cell receptor mutein in which the second specific binding affinity is greater than the first specific binding affinity.

52. A single-chain T cell receptor, wherein the single-chain T cell receptor is produced by increasing the specific binding affinity of a single-chain T cell receptor for a ligand, the method comprising:

determining a first specific binding affinity between the single-chain T cell receptor and the ligand,

infecting host cells with the bacteriophage library of claim 44, the infecting being under conditions which permit propagation of the bacteriophages,

contacting the host cells with the ligand sufficient to permit specific binding between at least one of the bacteriophages and the ligand to produce at least one specific binding complex between the bacteriophage and the ligand,

identifying one of the bacteriophages comprising the specific binding complex,

isolating DNA from the bacteriophage, the DNA comprising a sequence encoding a soluble fusion protein mutein and expressing the soluble fusion protein mutein,

separating a soluble single-chain T cell receptor mutein from the soluble fusion protein mutein,

determining a second specific binding affinity between the single-chain T cell receptor mutein and the ligand; and

identifying the single-chain T cell receptor with increased specific binding affinity for the ligand as the single-chain T cell receptor mutein in which the second specific binding affinity is greater than the first specific binding affinity.

53. A method of reducing binding between a T cell receptor and a ligand in a mammal, the method comprising:

administering to the mammal a therapeutically effective amount of the single-chain T cell receptor of claim 52.

54. A method of inducing an immune response in a mammal comprising administering to the mammal an effective amount of a single-chain T cell receptor cleaved from a soluble fusion protein comprising a bacteriophage coat protein covalently linked to the single-chain T cell receptor, wherein the immune response is capable of immunizing the mammal against T cell receptor epitopes on the surfaces of pathogenic T cells.

55. A method of preparing an antibody capable of specifically binding a T cell receptor, the method comprising administering to a mammal an effective amount of a single-chain T cell receptor cleaved from a soluble

fusion protein comprising a bacteriophage coat protein covalently linked to the single-chain T cell receptor.

56. A method of detecting a molecule capable of specifically binding a T cell receptor, the method comprising:

incubating the molecule with a bacteriophage display library under conditions sufficient to form a specific binding complex between the molecule and at least one bacteriophage in the library, the bacteriophage library comprising bacteriophages displaying fusion proteins, wherein each of the fusion proteins comprises a bacteriophage coat protein covalently linked to a single-chain T cell receptor; and

detecting the specific binding complex as indicative of the molecule capable of specifically binding the T cell receptor.

57. A molecule, wherein the molecule is produced by a method of detecting the molecule capable of specifically binding a T cell receptor, the method comprising:

incubating the molecule with a bacteriophage display library under conditions sufficient to form a specific binding complex between the molecule and at least one bacteriophage in the library, the bacteriophage library comprising bacteriophages displaying fusion proteins, wherein each of the fusion proteins comprises a bacteriophage coat protein covalently linked to a single-chain T cell receptor; and

detecting the specific binding complex as indicative of the molecule capable of specifically binding the T cell receptor.

58. A method of detecting a molecule capable of inhibiting specific binding between a ligand and a T cell receptor, the method comprising:

incubating a soluble fusion protein comprising a bacteriophage coat protein covalently linked to a single-chain T cell receptor, the incubating being in the presence of the ligand,

incubating a soluble fusion protein comprising a bacteriophage coat protein covalently linked to a single-chain T cell receptor, the incubating being in the presence of the ligand and the molecule; and

evaluating the interaction between the ligand and the soluble fusion protein in the absence and presence of the molecule,

wherein less interaction between the fusion protein and the ligand in the presence of the molecule than in the absence of the molecule is indicative of

the molecule capable of inhibiting specific binding between the ligand and the T cell receptor.

59. A molecule, wherein the molecule is produced by a method of detecting the molecule capable of inhibiting specific binding between a ligand and a T cell receptor, the method comprising:

incubating a soluble fusion protein comprising a bacteriophage coat protein covalently linked to a single-chain T cell receptor, the incubating being in the presence of the ligand,

incubating a soluble fusion protein comprising a bacteriophage coat protein covalently linked to a single-chain T cell receptor, the incubating being in the presence of the ligand and the molecule; and

evaluating the interaction between the ligand and the soluble fusion protein in the absence and presence of the molecule,

wherein less interaction between the fusion protein and the ligand in the presence of the molecule than in the absence of the molecule is indicative of the molecule capable of inhibiting specific binding between the ligand and the T cell receptor.

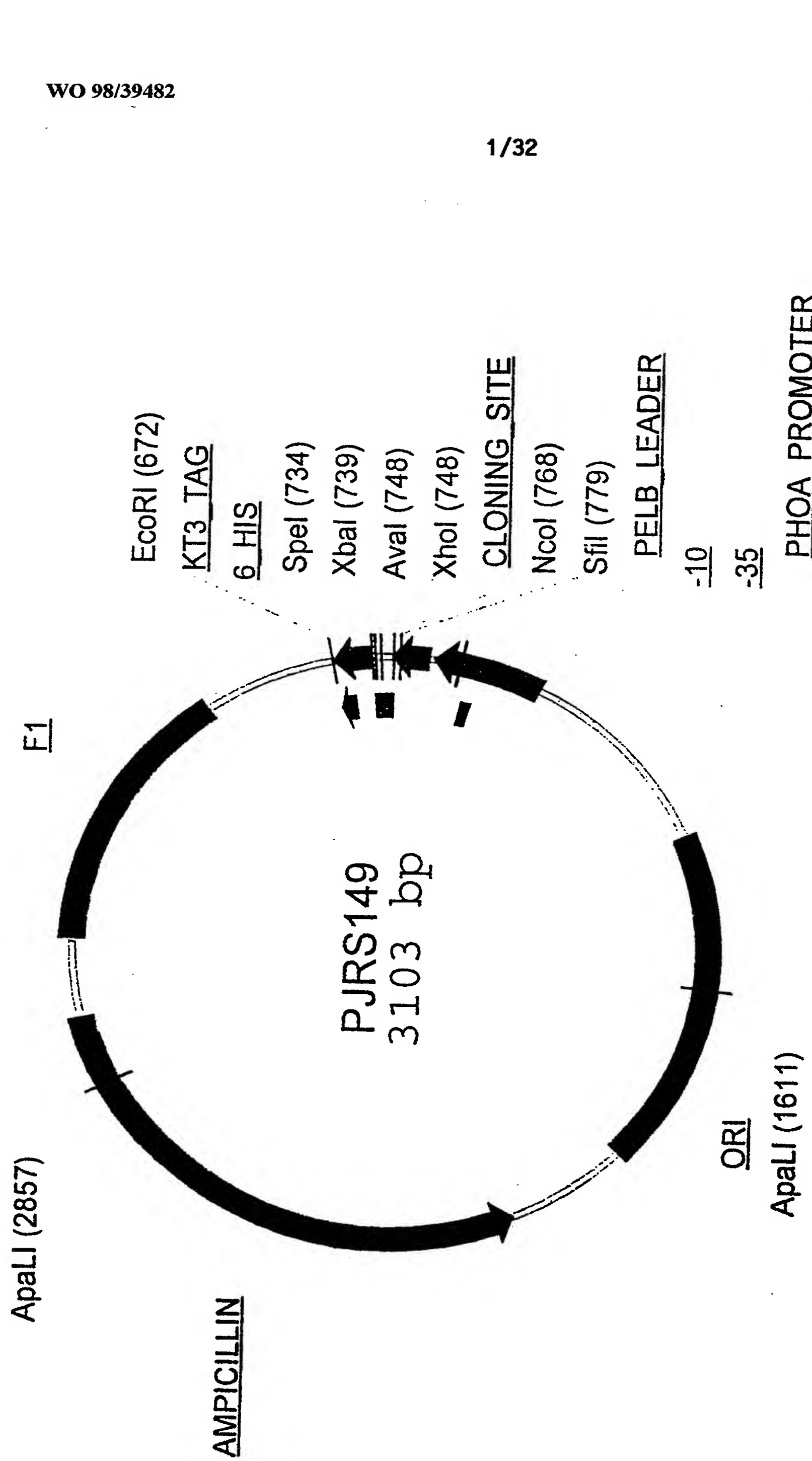

EcoRI (672)
KT3 TAG
6 HIS
SpeI (734)
XbaI (739)
AvaI (748)
XhoI (748)
CLONING SITE
NcoI (768)
SfiI (779)
PELB LEADER
-10
-35
PHOA PROMOTER
F1
PJRS149
3103 bp
ORI
ApaLI (1611)
ApaLI (2857)
AMPICILLIN

Fig. 1A

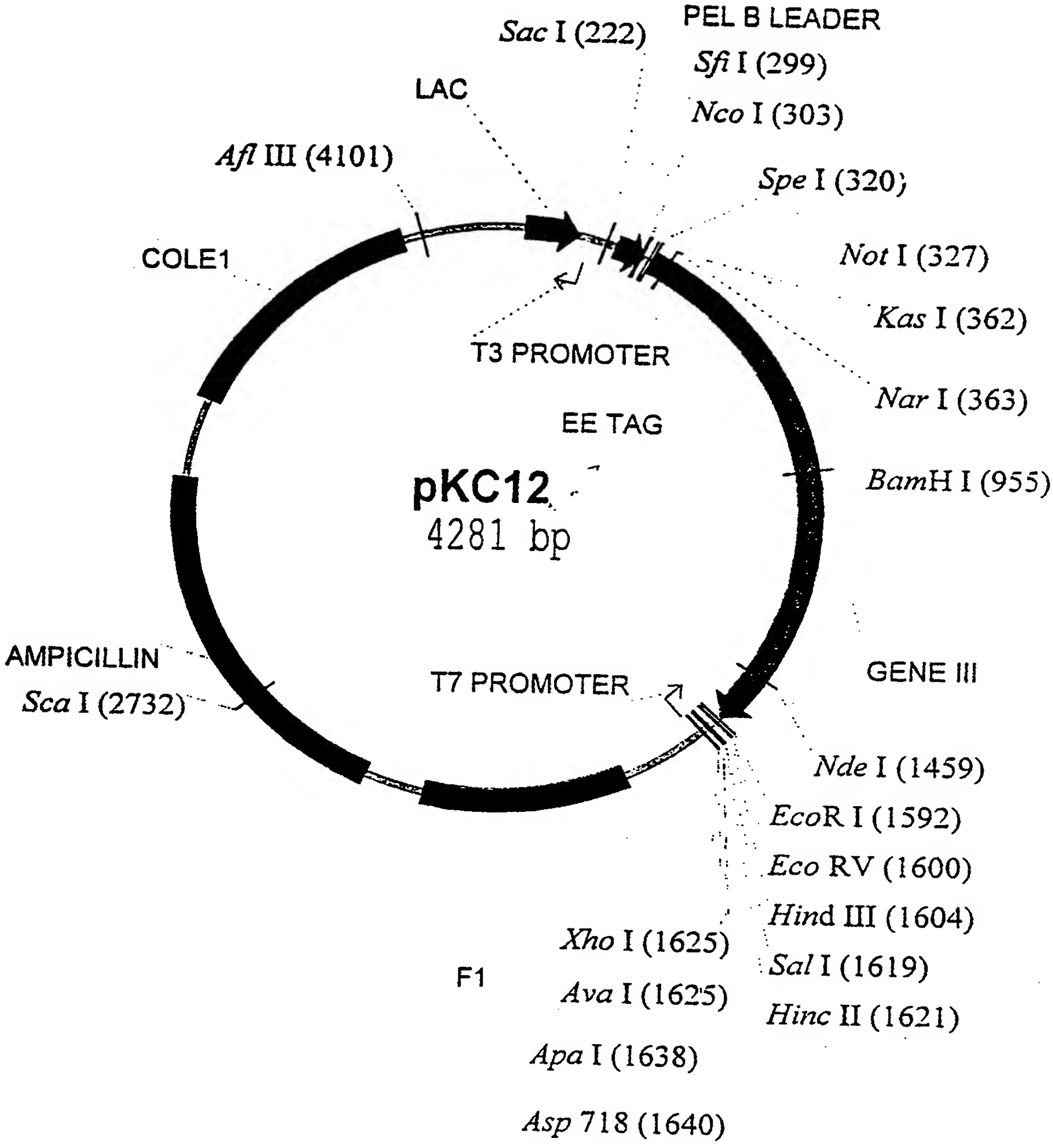

PEL B LEADER
Sac I (222)
Sfi I (299)
LAC
Nco I (303)
Afl III (4101)
Spe I (320)
COLE1
Not I (327)
Kas I (362)
T3 PROMOTER
Nar I (363)
EE TAG
pKC12
4281 bp
BamH I (955)
AMPICILLIN
T7 PROMOTER
GENE III
Sca I (2732)
Nde I (1459)
EcoR I (1592)
Eco RV (1600)
Hind III (1604)
Xho I (1625)
Sal I (1619)
F1
Ava I (1625)
Hinc II (1621)
Apa I (1638)
Asp 718 (1640)

Fig. 1B

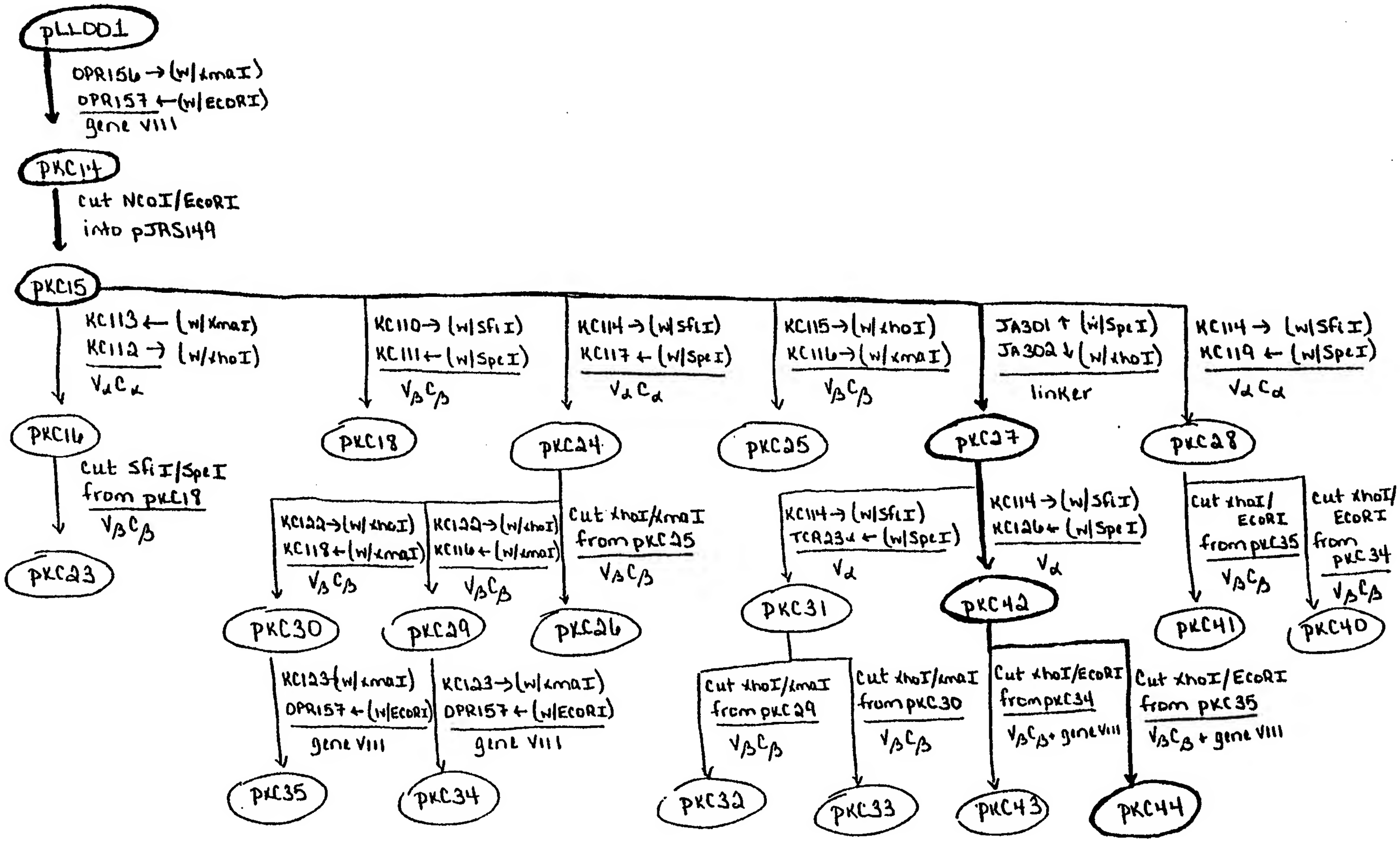
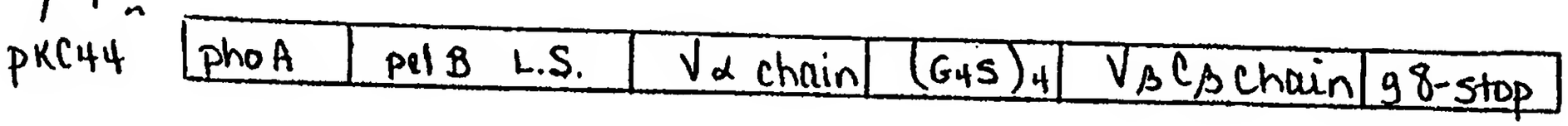
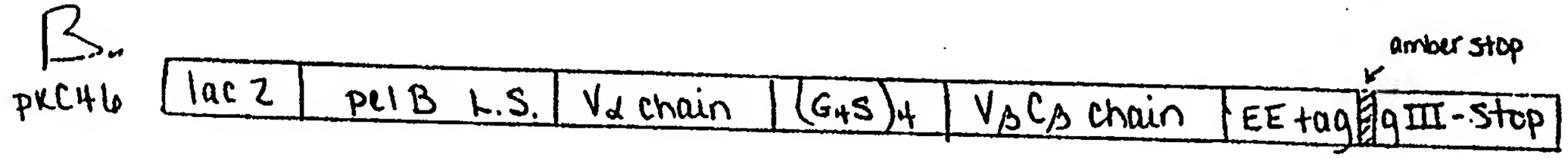

pLL001
OPR156 → (w/XmaI)
OPR157 ← (w/EcoRI)
gene VIII
pKC14
cut NcoI/EcoRI
into pJRS149
pKC15
KC113 ← (w/XmaI)
KC112 → (w/XhoI)
VαCα
KC110 → (w/SfiI)
KC111 ← (w/SpeI)
VβCβ
KC114 → (w/SfiI)
KC117 ← (w/SpeI)
VαCα
KC115 → (w/XhoI)
KC116 → (w/XmaI)
VβCβ
JA301 ↑ (w/SpeI)
JA302 ↓ (w/XhoI)
linker
KC114 → (w/SfiI)
KC119 ← (w/SpeI)
VαCα
pKC16
cut SfiI/SpeI
from pKC18
VβCβ
pKC23
pKC18
pKC24
pKC25
pKC27
pKC28
KC122 → (w/XhoI)
KC118 ← (w/XmaI)
VβCβ
KC122 → (w/XhoI)
KC116 ← (w/XmaI)
VβCβ
Cut XhoI/XmaI
from pKC25
VβCβ
pKC30
pKC29
pKC26
KC123 → (w/XmaI)
DPR157 ← (w/EcoRI)
gene VIII
KC123 → (w/XmaI)
DPR157 ← (w/EcoRI)
gene VIII
pKC35
pKC34
KC114 → (w/SfiI)
TCRβ3.4 ← (w/SpeI)
Vα
KC114 → (w/SfiI)
KC126 ← (w/SpeI)
Vα
pKC31
pKC42
Cut XhoI/XmaI
from pKC29
VβCβ
Cut XhoI/XmaI
from pKC30
VβCβ
Cut XhoI/EcoRI
from pKC34
VβCβ + gene VIII
Cut XhoI/EcoRI
from pKC35
VβCβ + gene VIII
pKC32
pKC33
pKC43
pKC44
Cut XhoI/
EcoRI
from pKC35
VβCβ
Cut XhoI/
EcoRI
from
pKC34
VβCβ
pKC41
pKC40

Fig. 2

A.


pKC44
phoA
pelB L.S.
Vα chain
(G4S)4
VβCβ chain
g8-stop

B.


pKC46
lac Z
pelB L.S.
Vα chain
(G4S)4
VβCβ chain
EE tag
amber stop
gIII-Stop

C.

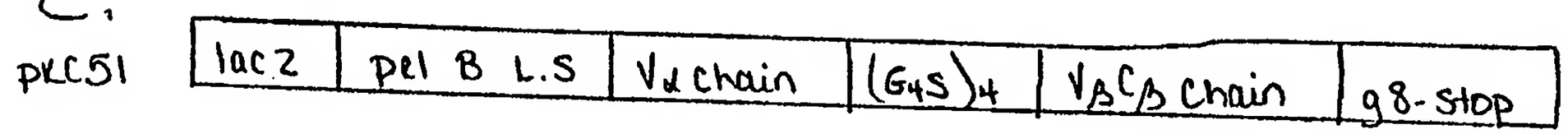

pKC51
lac Z
pelB L.S
Vα chain
(G4S)4
VβCβ chain
g8-stop

Fig. 3

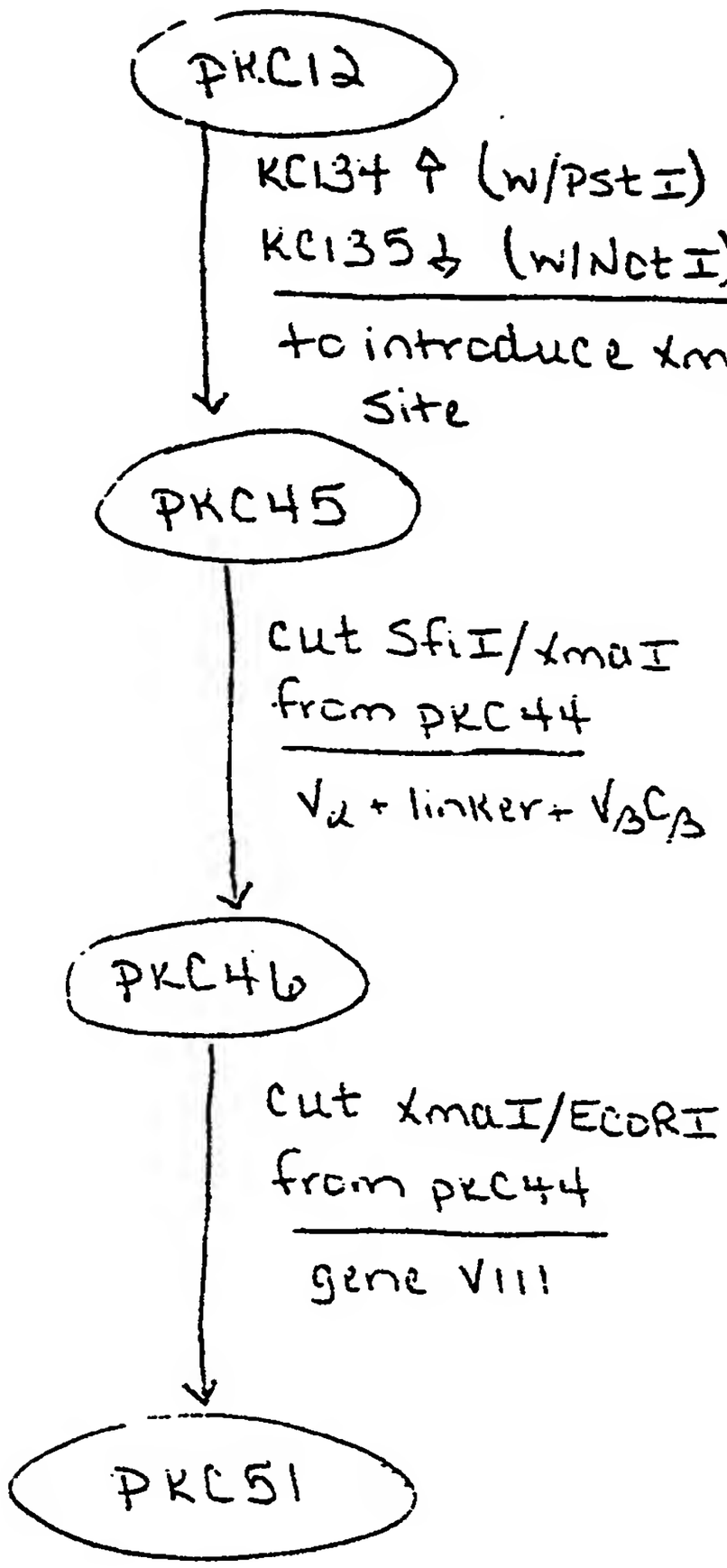

PKC12
KC134 ↑ (w/PstI)
KC135 ↓ (w/NotI)
to introduce XmaI Site
PKC45
Cut SfiI/XmaI from pKC44
V_α + linker + $V_\beta C_\beta$
PKC46
Cut XmaI/EcoRI from pKC44
gene VIII
PKC51

Fig. 4

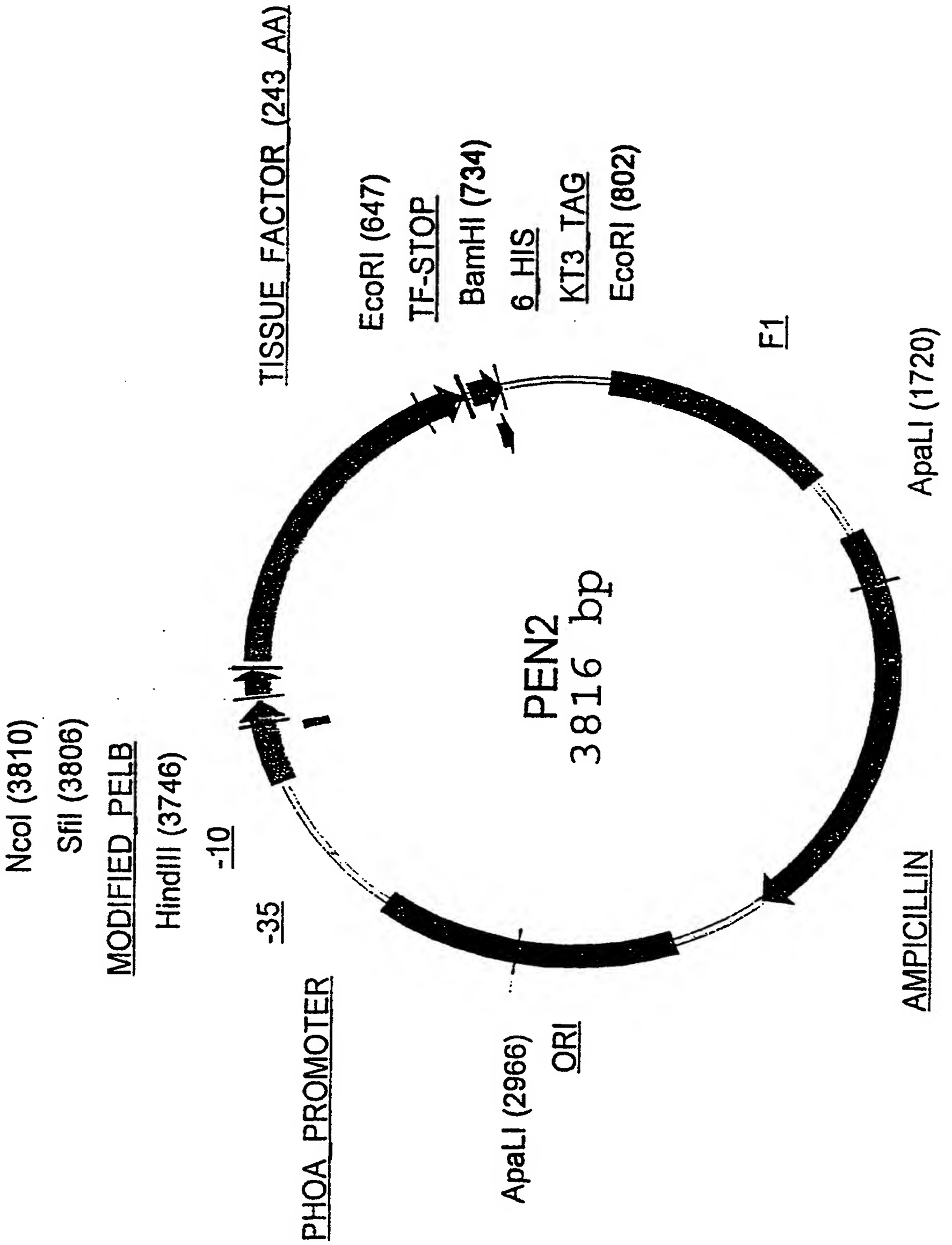
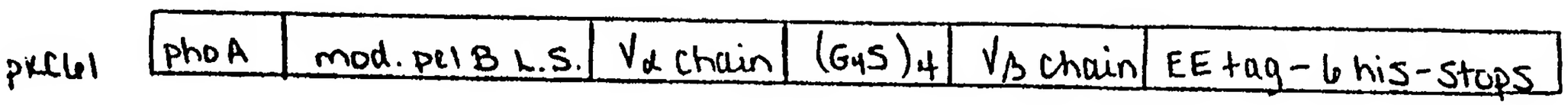
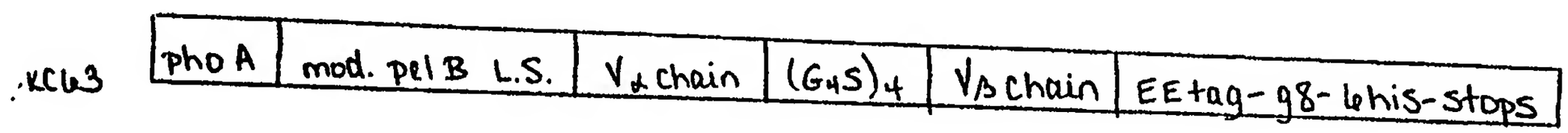

TISSUE FACTOR (243 AA)
EcoRI (647)
TF-STOP
BamHI (734)
6 HIS
KT3 TAG
EcoRI (802)
F1
ApaLI (1720)
NcoI (3810)
SfiI (3806)
MODIFIED PELB
HindIII (3746)
-10
-35
PHOA PROMOTER
ApaLI (2966)
ORI
PEN2
3816 bp
AMPICILLIN

Fig. 5


pKC61
phoA
mod. pelB L.S.
Vα chain
(G4S)4
Vβ chain
EE tag - 6 his - stops


pKC63
phoA
mod. pelB L.S.
Vα chain
(G4S)4
Vβ chain
EE tag - g8 - 6 his - stops

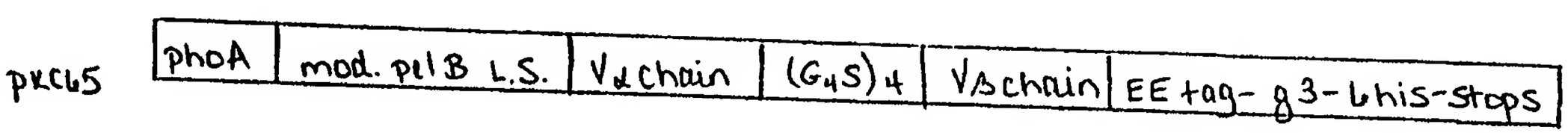

pKC65
phoA
mod. pelB L.S.
Vα chain
(G4S)4
Vβ chain
EE tag - g3 - 6 his - stops

Fig. 6A

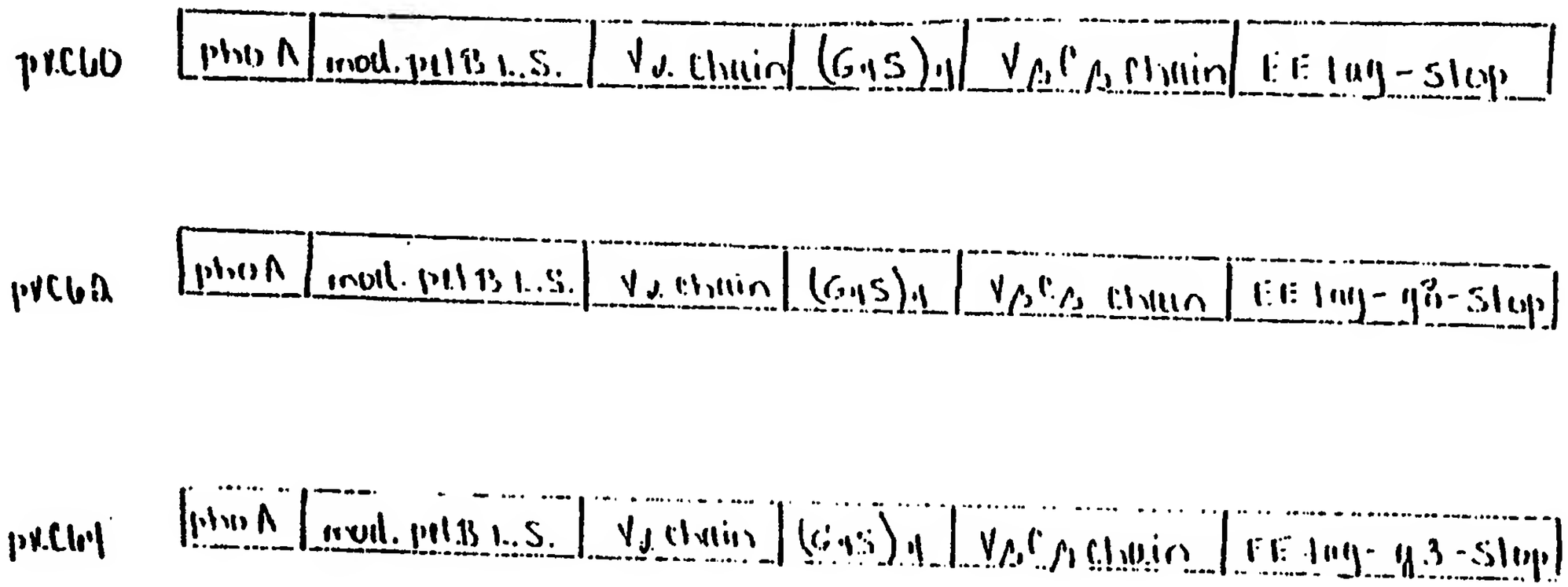

pYC60
phoA
mod. pelB L.S.
VH chain
(Gly4Ser)4
VL CA chain
EE tag - stop
pYC62
phoA
mod. pelB L.S.
VH chain
(Gly4Ser)4
VL CA chain
EE tag - g3 - stop
pYC64
phoA
mod. pelB L.S.
VH chain
(Gly4Ser)4
VL CA chain
EE tag - g3 - stop
pYC66
phoA
mod. pelB L.S.
VH CA chain
(Gly4Ser)4
VL CA chain
EE tag - g3 - stop
pYC68
phoA
mod. pelB L.S.
VH CA chain
(Gly4Ser)4
VL CA chain
EE tag - stop

Fig. 6B

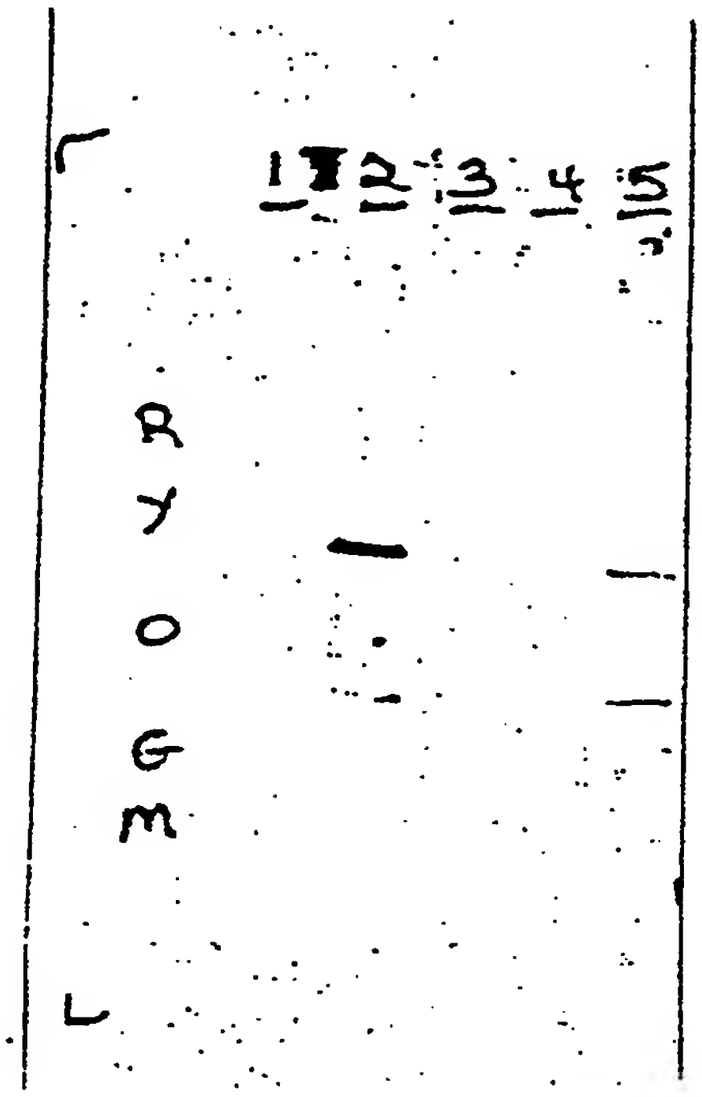


Fig. 7

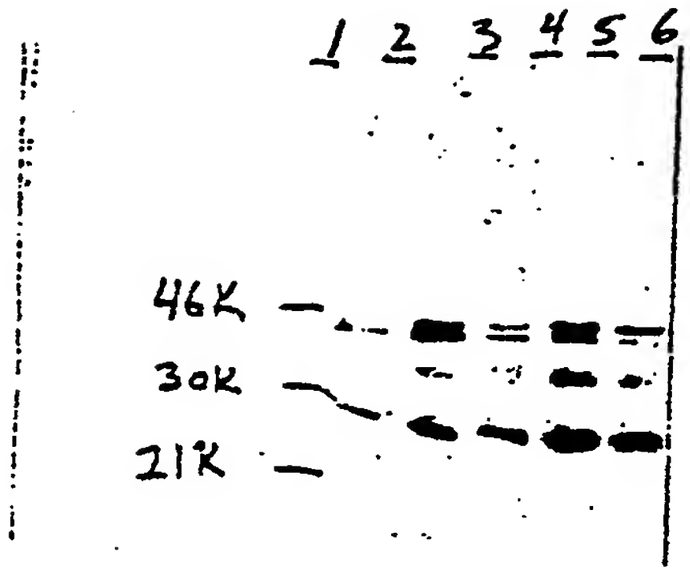


Fig. 8

Affinity Purification of scTCR/geneVIII Fusion Protein

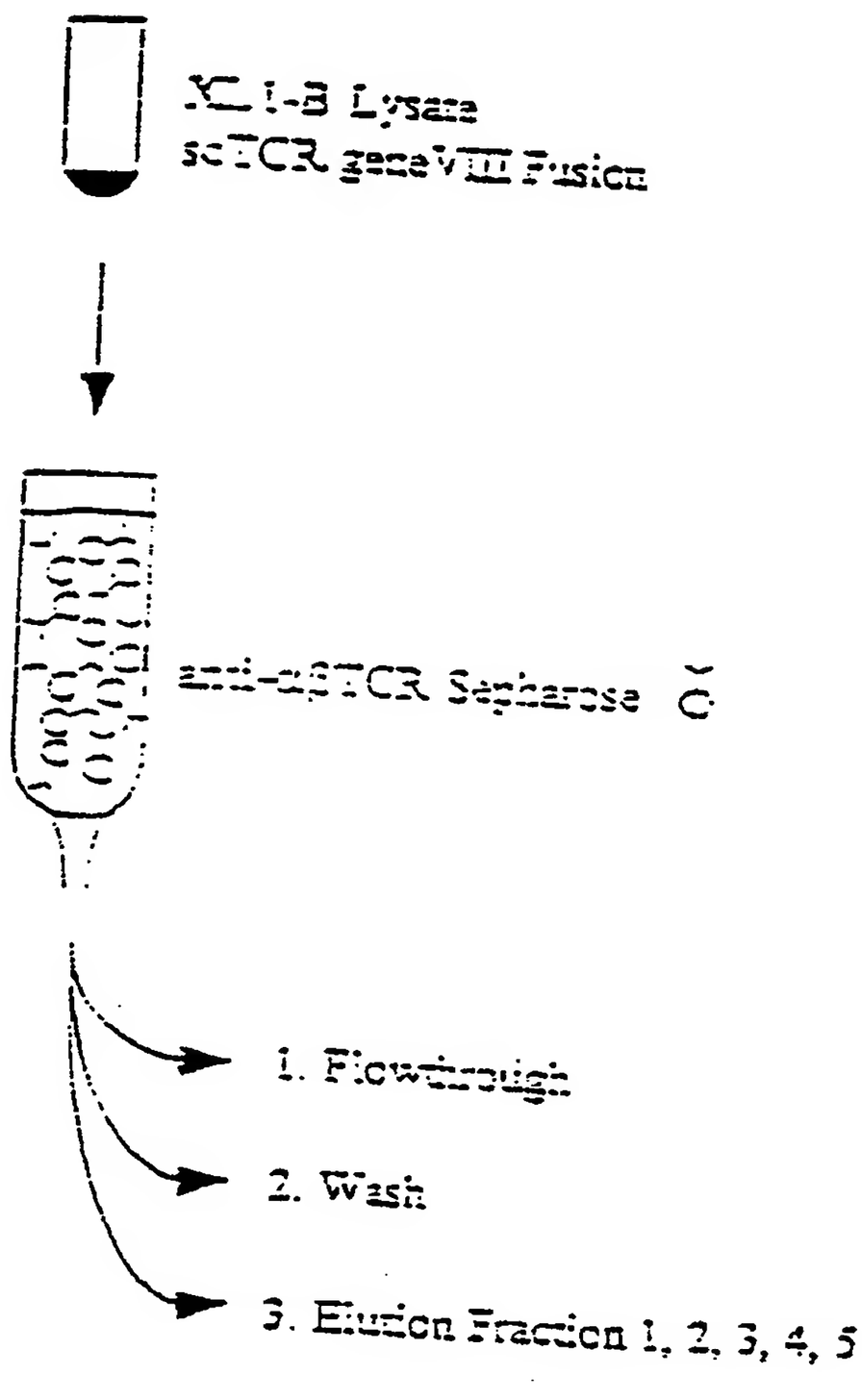


Fig. 9

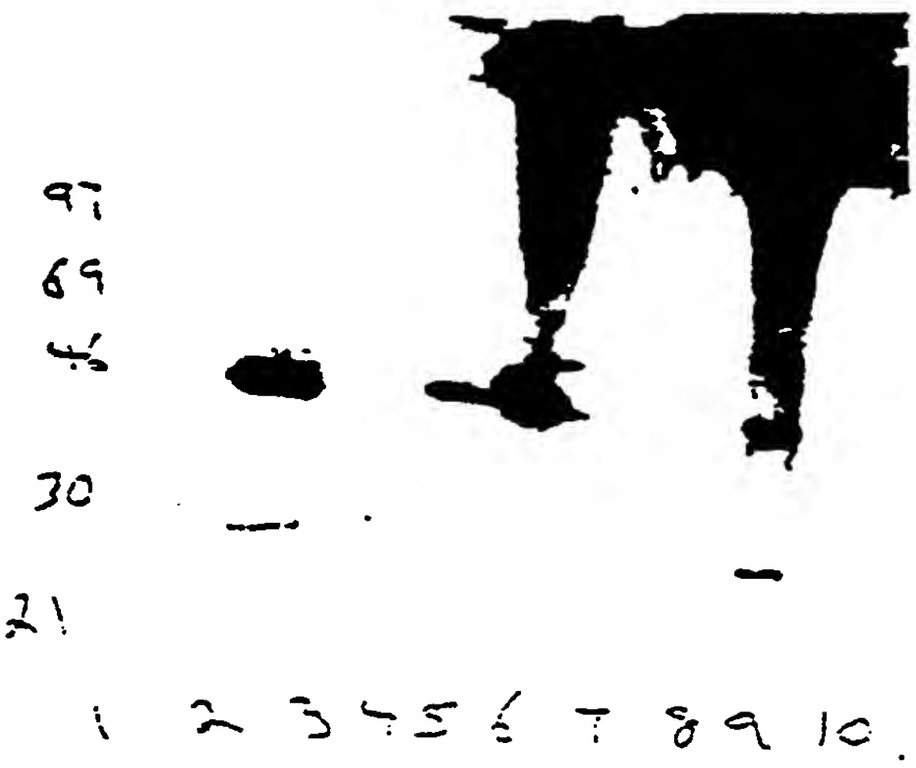


Fig. 10

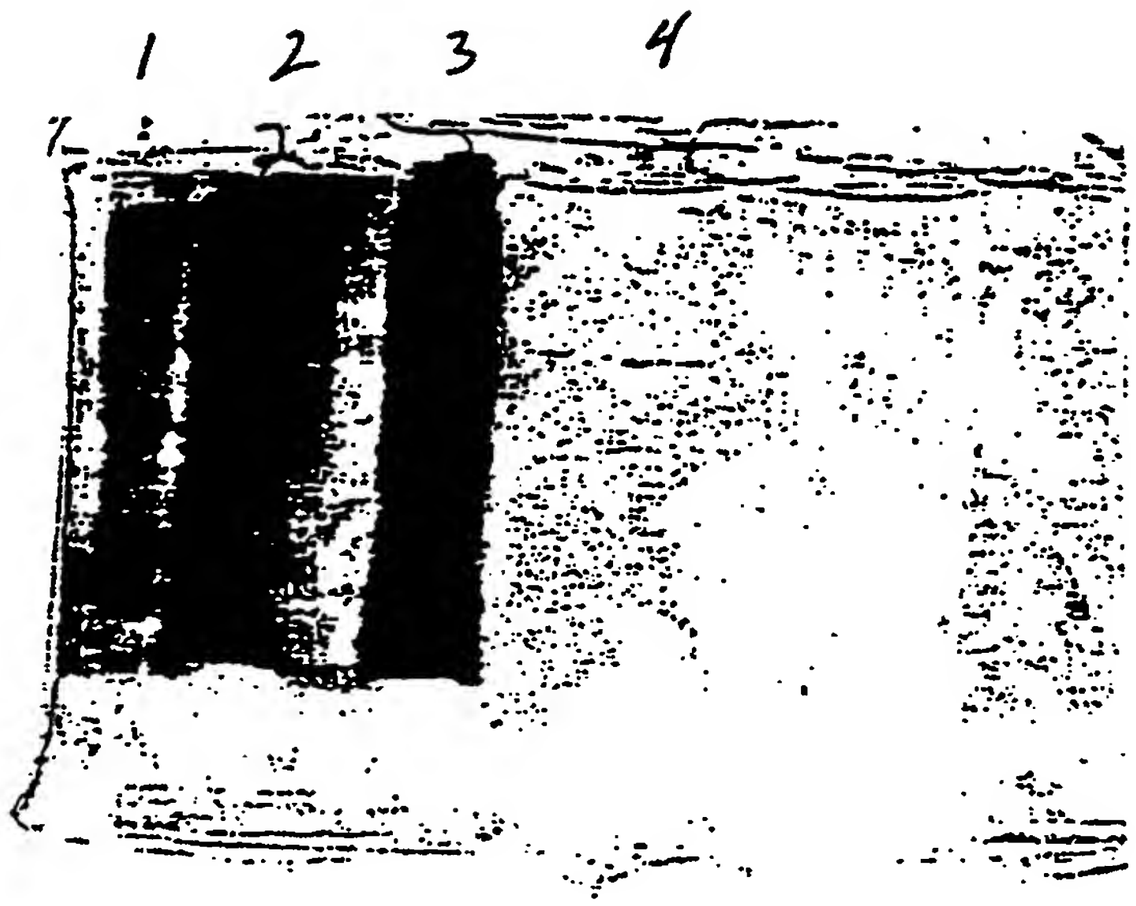


Fig. 11

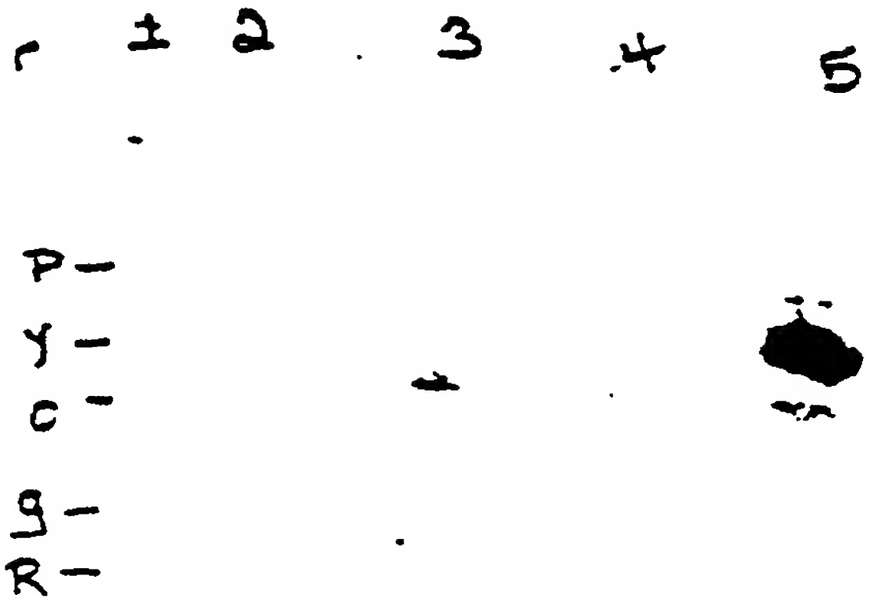


Fig. 12

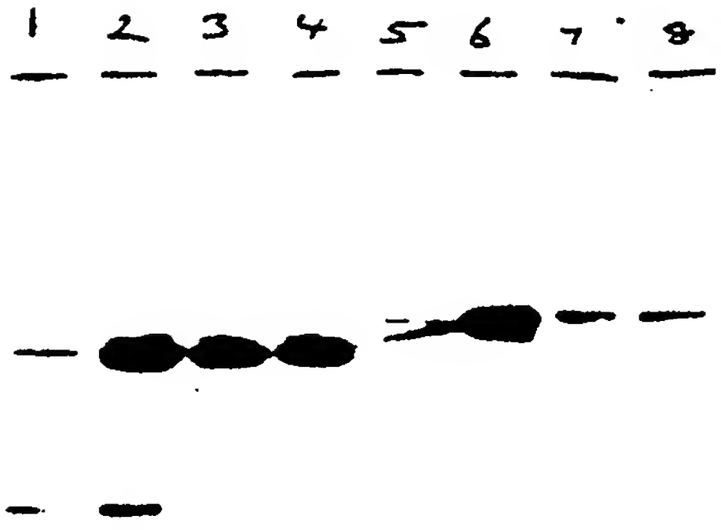


Fig. 13

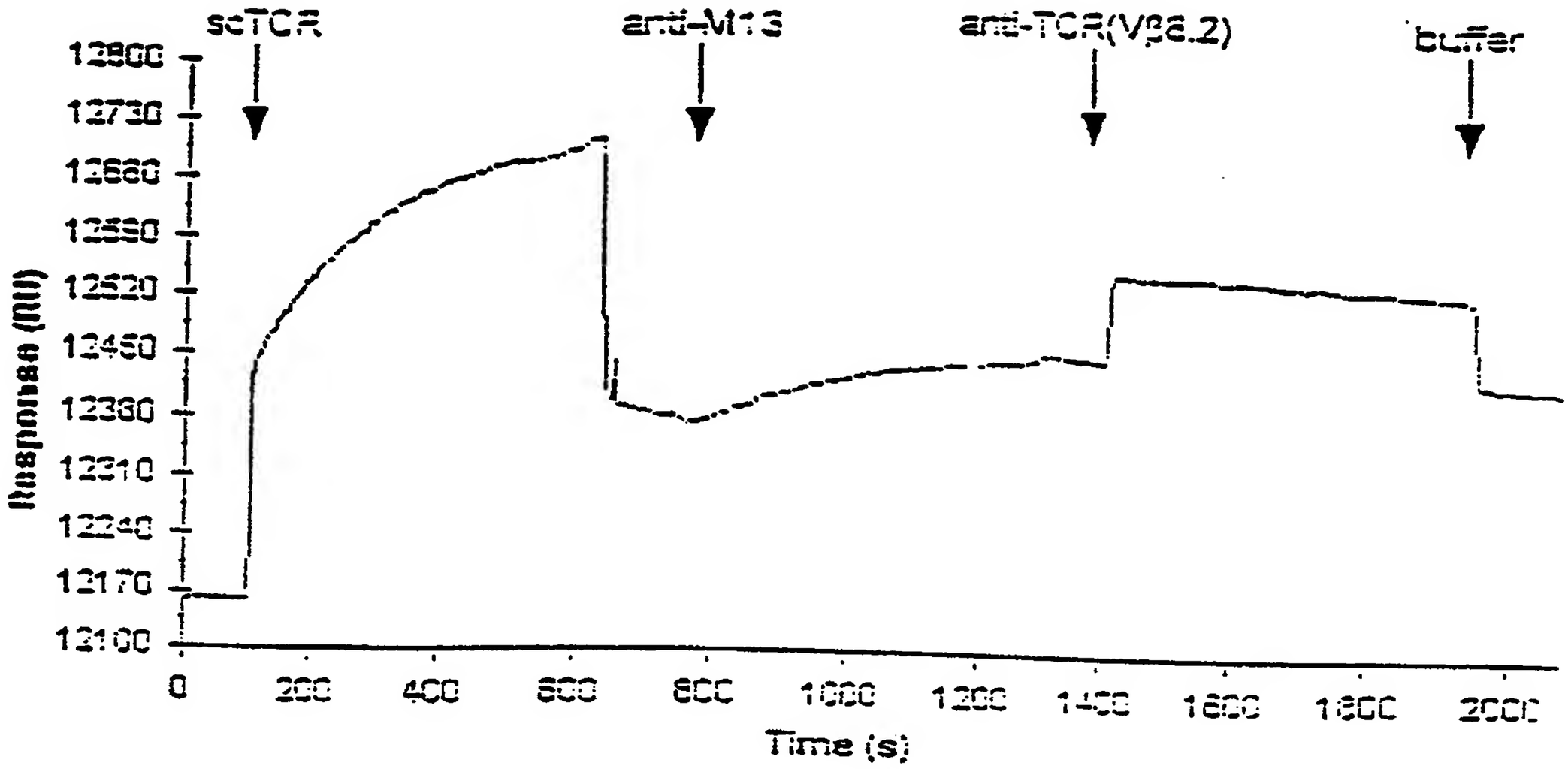

Injections:
scTCR
anti-M13
anti-TCR(Vβ8.2)
buffer
12800
12730
12660
12590
12520
12450
12380
12310
12240
12170
12100
Response (RU)
0
200
400
600
800
1000
1200
1400
1600
1800
2000
Time (s)

Fig. 14

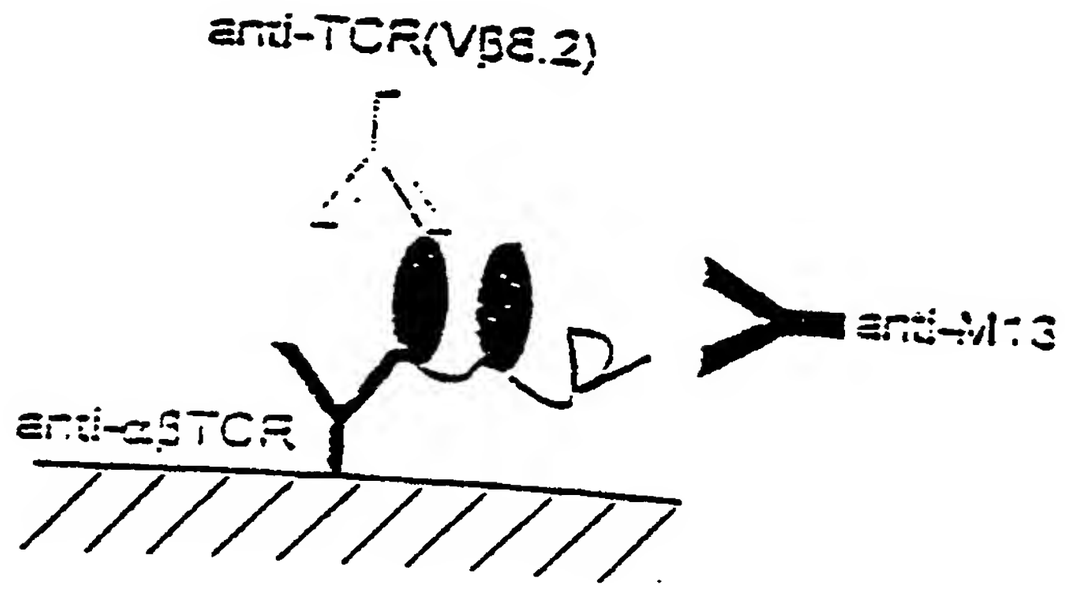


Fig 15

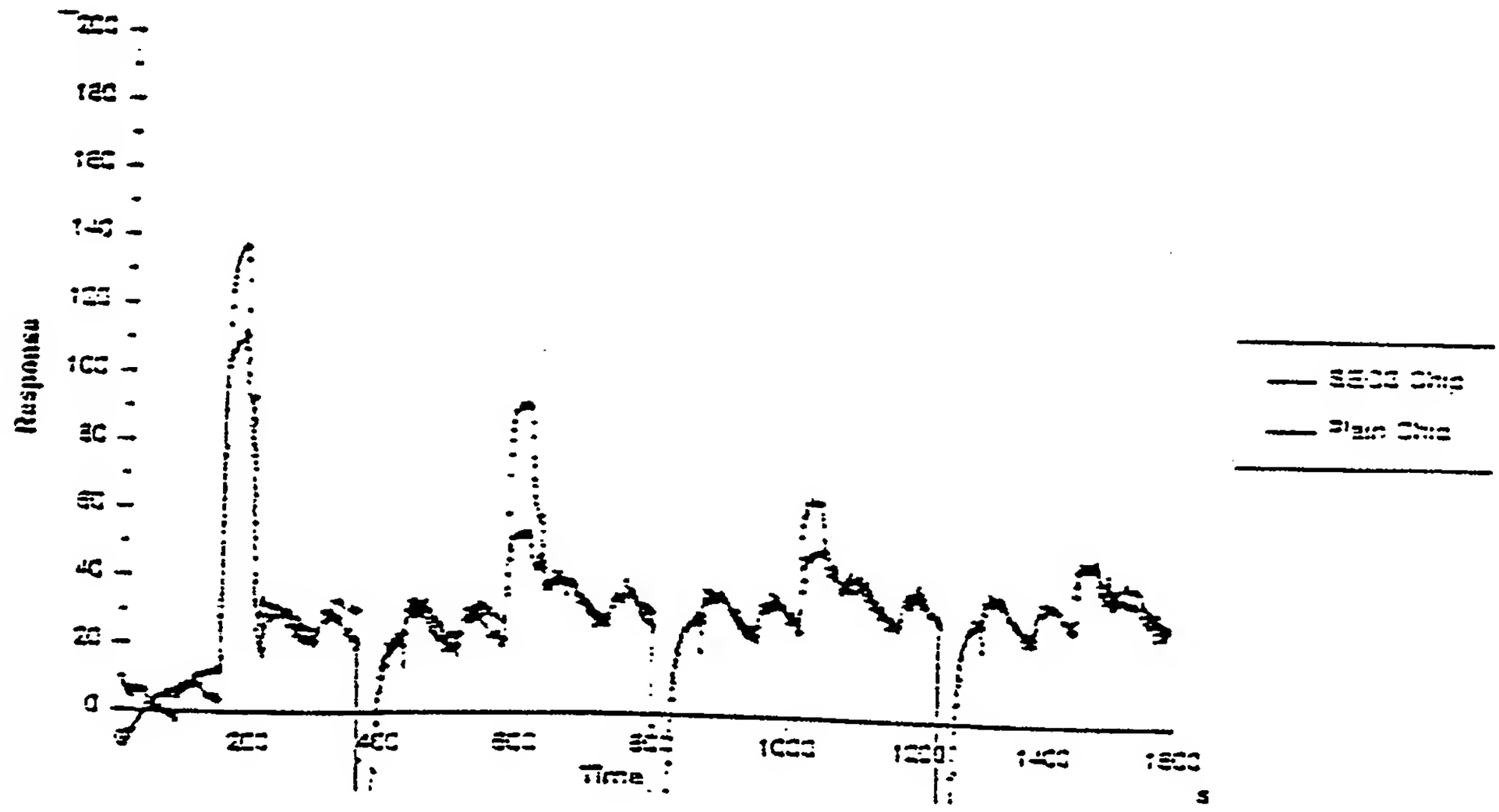


Fig. 16

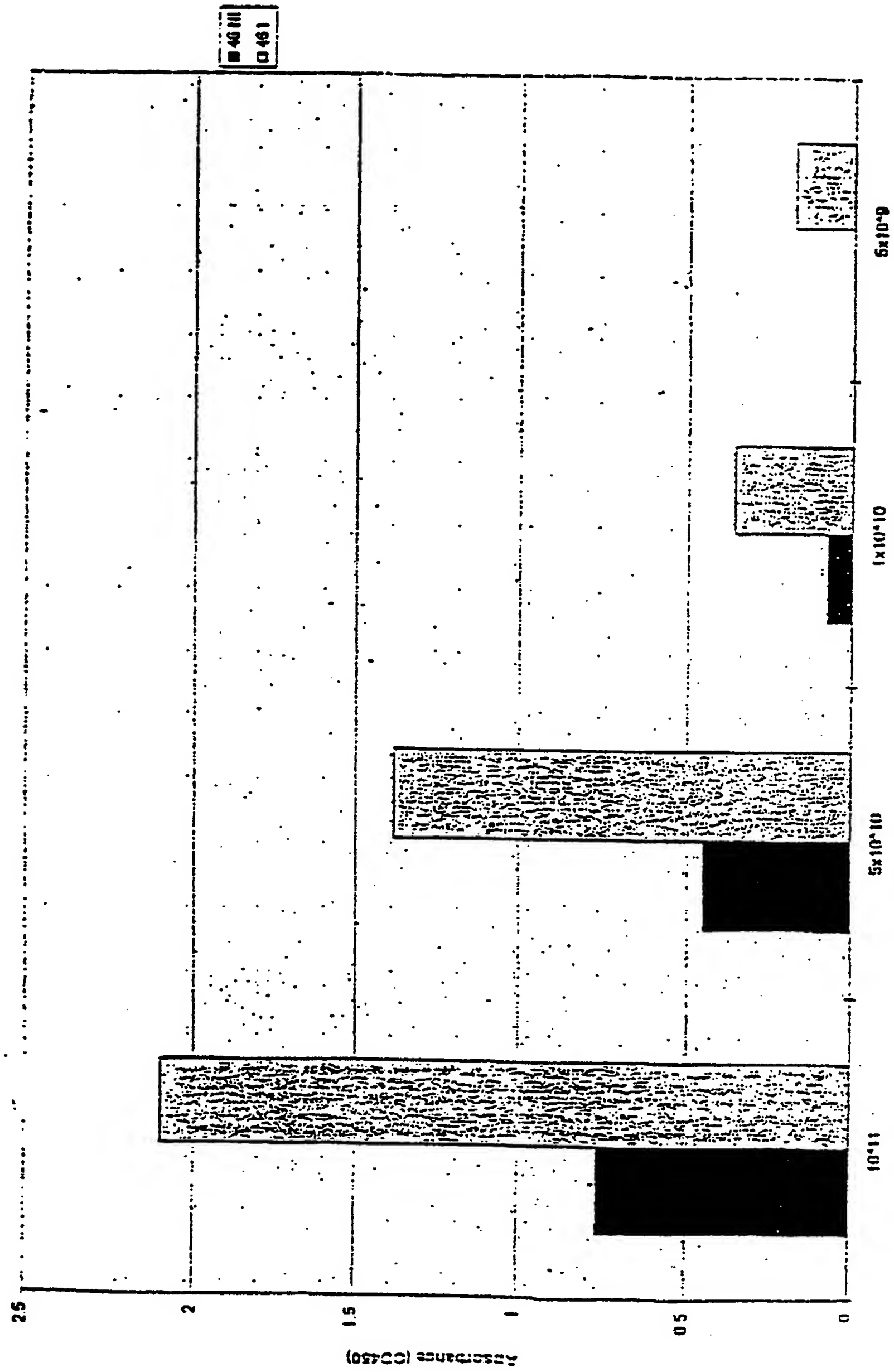

40 III
46 I
5x10^9
1x10^10
clubwell
5x10^10
10^11
2.5
2
1.5
1
0.5
0
Absorbance (OD450)

Fig. 17

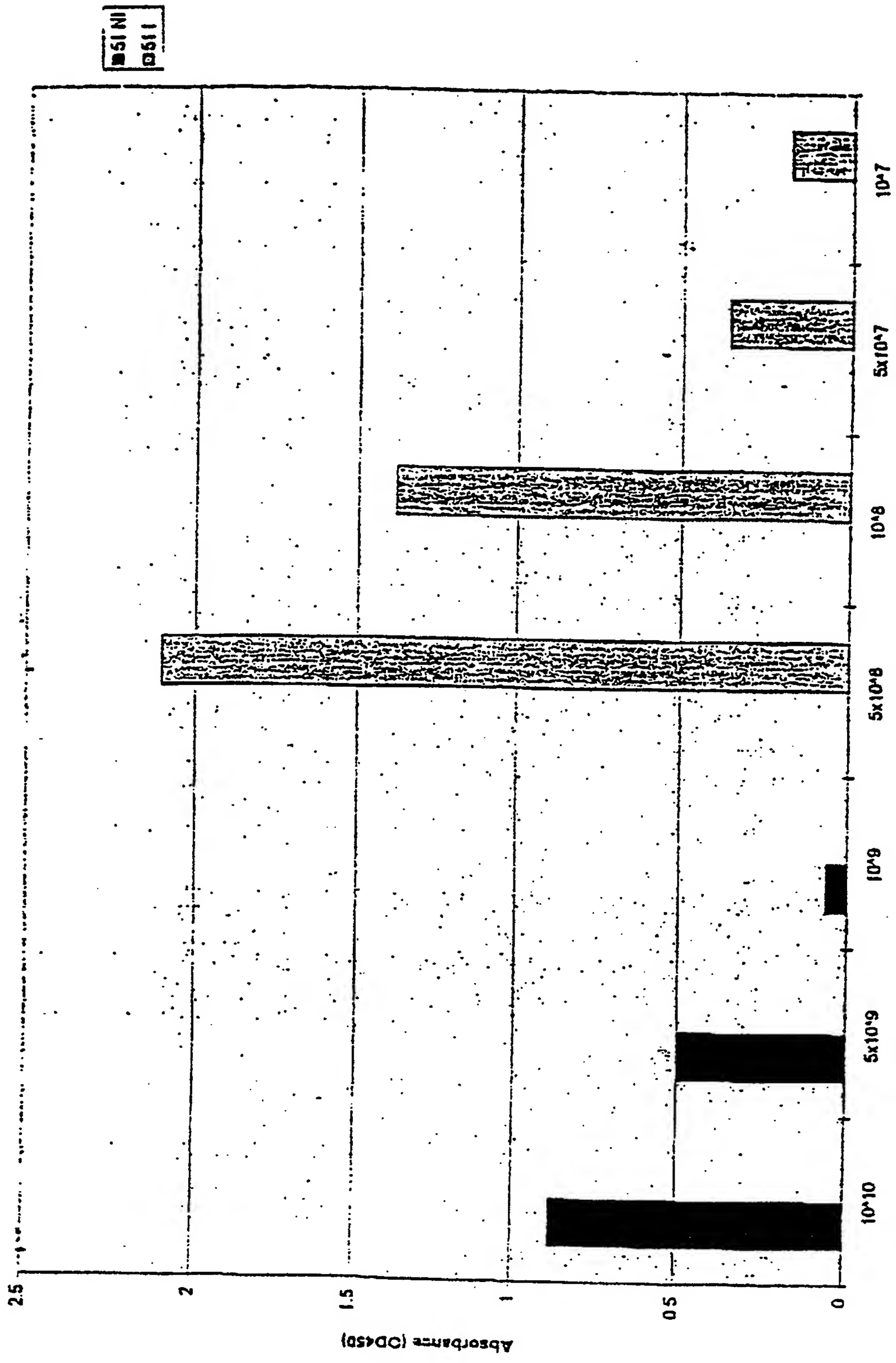

Si NI
Si I
10^7
5x10^7
10^8
5x10^8
10^9
5x10^9
10^10
cfu/well
2.5
2
1.5
1
0.5
0
Absorbance (OD450)

Fig. 18

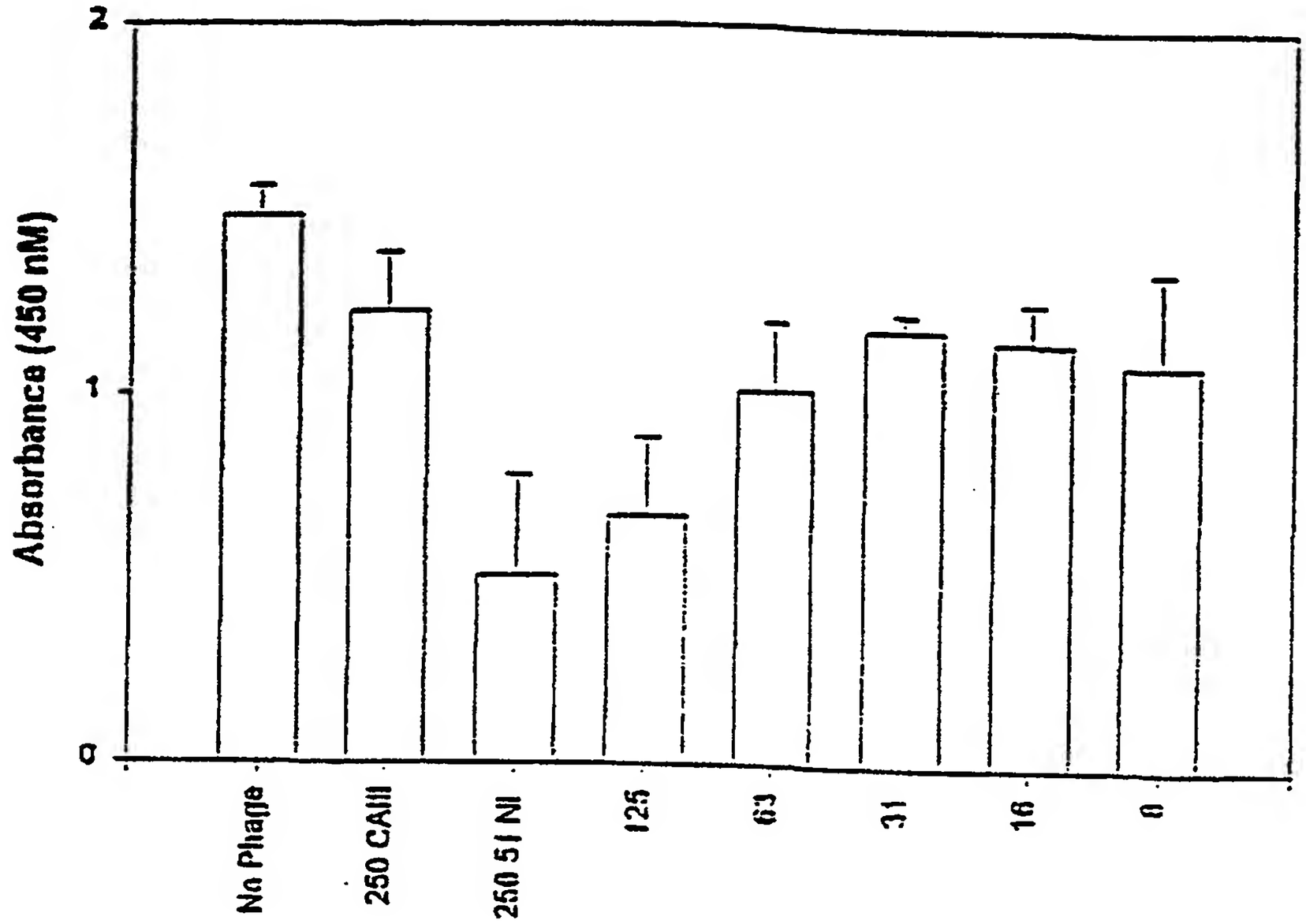

Absorbance (450 nM)
2
1
0
No Phage
250 CAIII
250 5I NI
125
63
31
16
0
Phage Titer (CFU/Well) x10^10

Fig. 19-A

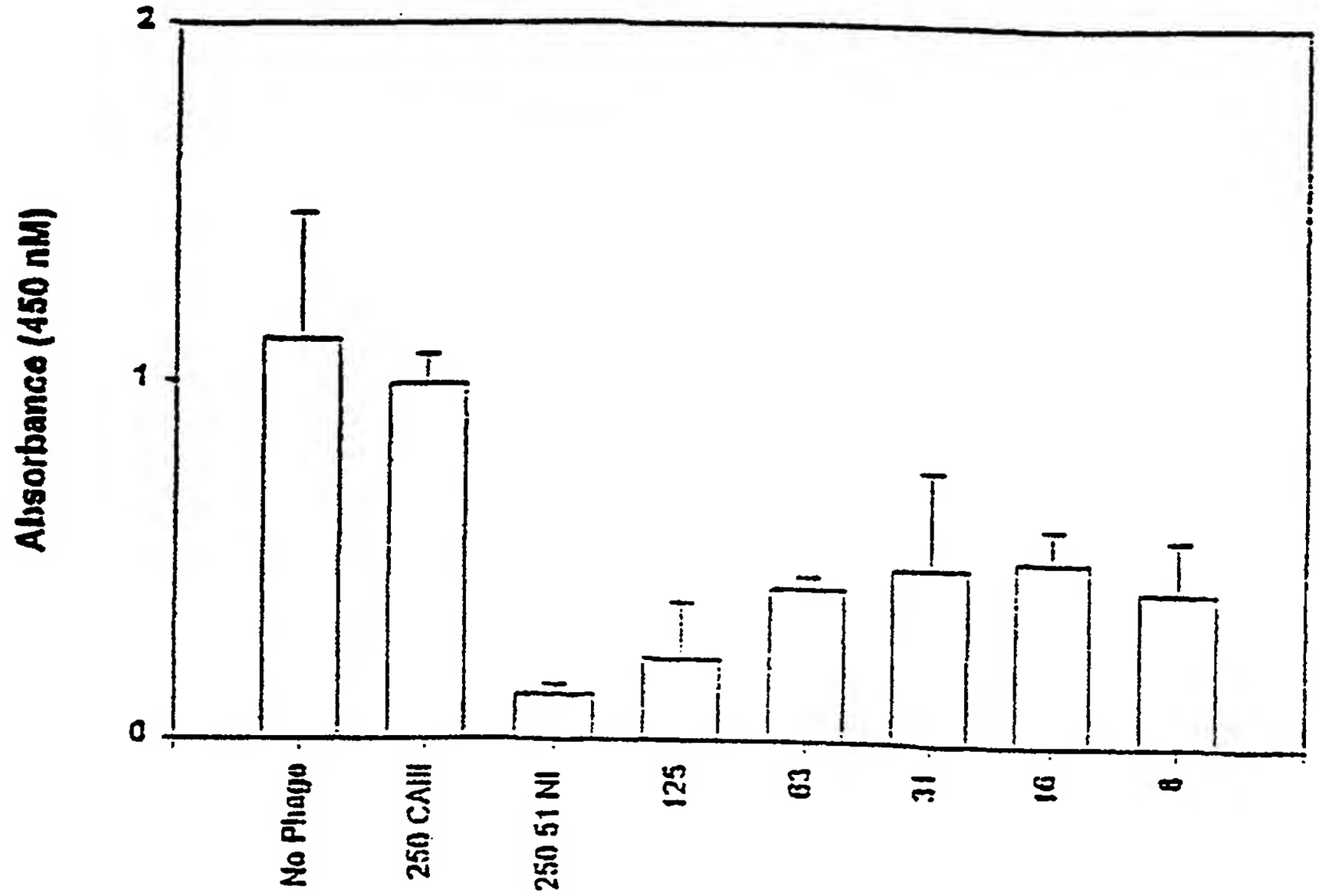

Absorbance (450 nM)
2
1
0
No Phage
250 CAIII
250 51 NI
125
63
31
16
8
Phage Titer (CFU/Well) x10^10

Fig. 19-B

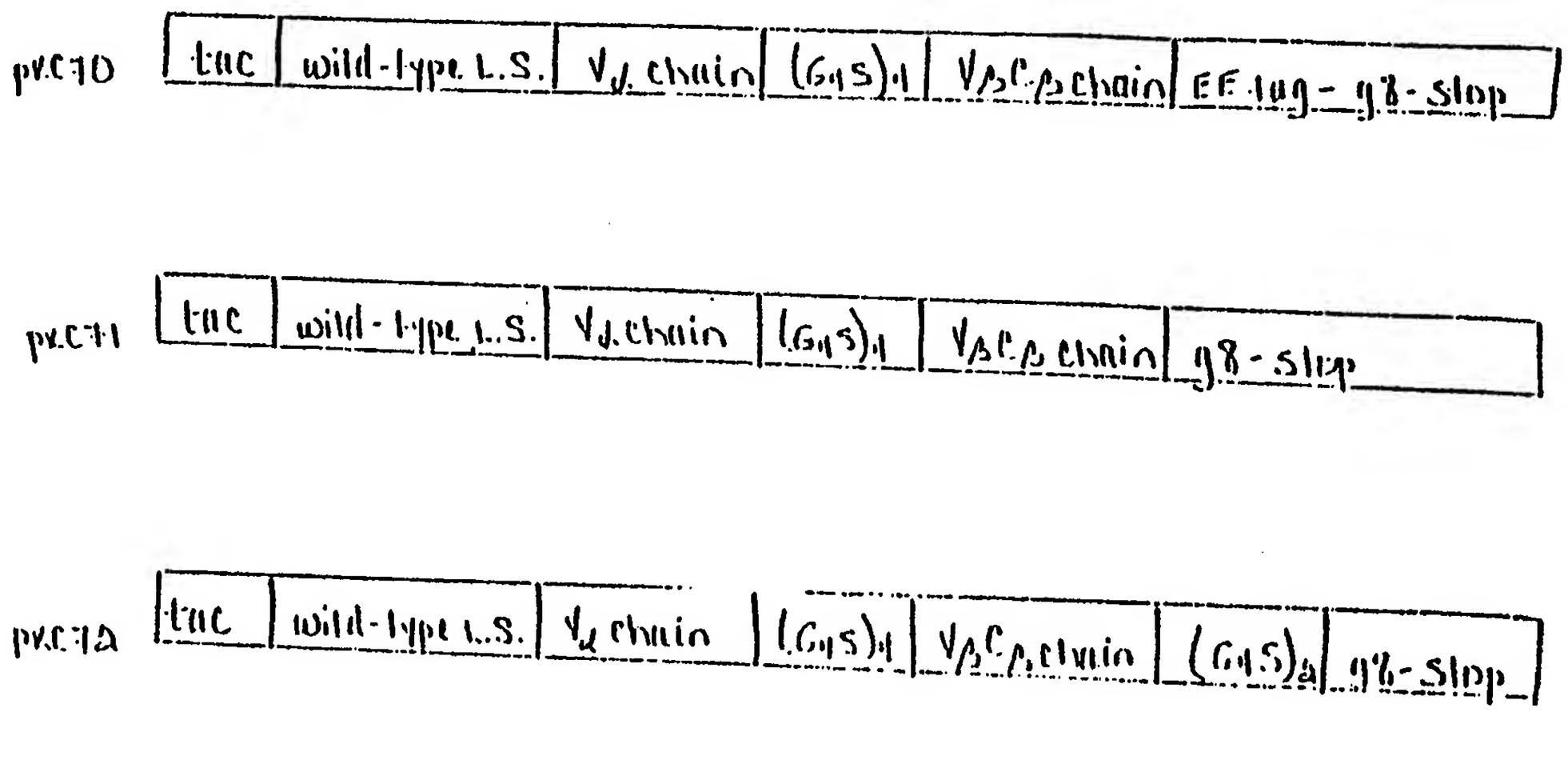

pvc10
tac
wild-type L.S.
V_H chain
$(Gly_4Ser)_4$
$V_\beta C_\beta$ chain
EE tag - g8-stop
pvc11
tac
wild-type L.S.
V_H chain
$(Gly_4Ser)_4$
$V_\beta C_\beta$ chain
g8-stop
pvc19
tac
wild-type L.S.
V_H chain
$(Gly_4Ser)_4$
$V_\beta C_\beta$ chain
$(Gly_4Ser)_3$
g8-stop

Fig. 20

Primer	Seq Id No	Sequence (5' to 3')
KC100	001	CGG CCA TGG CCC AGC TGC AGA CTA GTG C
KC101	002	GGC CGC ACT AGT CTG CAG CTG GGC CAT GGC CGG CT
KC110	003	CTC GCG GCC CAG CCG GCC ATG GCC GAG GCT GCA GTC ACC CAA AGC
KC111	004	CTT CCT CAC TAG TAC AGT CTG CTC GGC CCC AG
KC112	005	GAT GGC CTC GAG GAG CAG GTG GAG CAG CTT
KC113	006	GAC TAG CCC GGG ACA GGG AAC GTC TGA ACT GGG
KC114	007	CTC GCG GCC CAG CCG GCC ATG GCC GAG CAG GTG GAG CAG CTT CCT
KC115	008	CTC GCG CTC GAG GAG GCT GCA GTC ACC CAA AGC
KC116	009	CTC GCG CCC GGG ACA GTC TGC TCG GCC CCA GGC
KC117	010	CTC GCG ACT AGT ACA GGG AAC GTC TGA ACT GGG
KC118	011	CTC GCG CCC GGG GTC TGC TCG GCC CCA GGC
KC119	012	CTC GCG ACT AGT GGG AAC GTC TGA ACT GGG
KC120	013	CTC GCG ACT AGT GTC TGC TCG GCC CCA GGC
KC121	014	CTC GCG CCC GGG GGG AAC GTC TGA ACT GGG
KC122	015	CTC GCG CTC GAG CGA GGC TGC AGT CAC CCA AAG C
KC123	016	GGG GGG CCC GGG GCT GAG GGT GAC GAT CCC GCA AAA G

Fig. 21A

Primer	Seq Id No	Sequence (5' to 3')
KC124	017	CTA GTC TGG TGG CGG TGG CAG CGG CGG TGG TGG TTC CGG TGG CGG CGG TTC TGG CGG TGG CGG TTC C
KC125	018	TCG AGG AAC CGC CAC CGC CAG AAC CGC CGC CAC CGG AAC CAC CAC CGC CGC TGC CAC CGC CAC CAG A
KC126	019	GTG CTC ACT AGT GTT TGG CTC TAC AGT GAG TTT GGT G
KC127	020	GAT GGC TCG AGT GAG CAG GTG GAG CAG CTT CCT
KC128	021	CTA GTC CCC GGG TAC AAC TGT GAG TCT GGT TCC
KC129	022	CTC GAG ACT AGT TAC AAC TGT GAG TCT GGT TCC
KC130	023	CGG CCG AGG AAG AAG AGT ACA TCC CGA TGG ATC
KC131	024	GGG CCA TCC ATC GGG ATG TAC TCT TCT TCC TCG GCC GGC T
KC132	025	CCG GGG AGG AAG AAG AGT ACA TCC CGA TGG ATT GAG
KC133	026	AAT TCT CAA TCC ATC GGG ATG TAC TCT TCT TCC TCC
KC134	027	GCC CGG GAC TAG TGC
KC135	028	GGC CGC ACT AGT CCC GGG CTG CA
KC136	029	CTA GTC CCC GGG TCA TCA AGC GGC GCC TTC CAT CGG CAT GTA CTC TTC TTC CTC TAC AAC TGT GAG TCT GGT TCC
KC137	030	CTA GTC CCC GGG TCA TCA AGC GGC GCC TTC CAT CGG CAT GTA CTC TTC TTC CTC GTC TGC TCG GCC CCA GGC

Fig. 21 B

Primer	Seq Id No	Sequence (5' to 3')
KC138	031	CTA GTC CCC GGG TAC AAC TGT GAG TCT GGT TCC
KC139	032	CCG GGG AGG AAG AAG AGT ACA TGC CGA TGG AAG GCG CCG CTT AGC
KC140	033	CCT CCT TCT TCT CAT GTA CGG CTA CCT TCC GCG GCG AAT CGG GCC
KC141	034	GAT CAG CCC GGG GAG GCT GCA GTC ACC CAA AGC
KC142	035	CTA GTC CCC GGG ACA GTC TGC TCG GCC CCA CCG
KC143	036	CCG GGG AGG AAG AAG AGT ACA TGC CGA TGG AAG GCG CCG CTC
KC144	037	CCT CCT TCT TCT CAT GTA CGG CTA CCT TCC GCG GCG AGG GCC
KC145	038	CGC CGC TCA CCA TCA CCA TCA TCA CTG ATG AC
KC146	039	GGC GAG TGG TAG TGG TAG TAG TGA CTA CTG GGC C
KC147	040	GAT CAG GGC GCC GCT ACT GTT GAA AGT TGT TTA
KC148	041	CTG ATC GGA TCC TCA TTA AAG CCA GAA TGG AAA
KC149	042	CCG GGC TAA GCG GCG CCT TCC ATC GGC ATG TAC TCT TCT TCC TCC
KC150	043	CCG GGA GCG GCG CCT TCC ATC GGC ATG TAC TCT TCT TCC TCC
KC151	044	CCG GGT CAT CAG TGA TGA TGG TGA TGG TGA GCG G
KC152	045	GCT CGA GCT TAC TCC

Fig. 21C

Primer	Seq Id No	Sequence (5' to 3')
KC153	046	CGC TCA TTA GGC GG
KC154	047	GTG TAC TTC TGT GCC
KC155	048	CTG TGA GTC TGG TTC
KC156	049	GCA GGT TCT GGG TTC
KC157	050	CAT TTA CTA ACG TCT GG
KC158	051	CGC CTG GTA CTG AGC
KC159	052	CCT CAA CCT CCT GTC
KC160	053	CTT ATT CCG TGG TGT C
KC161	054	CCA CCC TCA GAA CCG
KC162	055	GAA TTT ACC GTT CCA G
KC163	056	CTT TAG CGT CAG ACT G
KC164	057	GAA ACG CAA AGA CAC C
OPR156	058	GGG GGG CCC GGG CTG CTG AGG GTG ACG ATC CCG CAA AAG
OPR157	059	GGG GGG GAA TTC TAT TAG CTT GCT TTC GAG GTG AAT TTC
JWTCR222	060	GAG CAC GGC CCA GCC GGC CAT GGC CGA GGC TGC AGT CAC CC
JWTCR221	061	GAG CAC GAG ACT AGT AGC ACG AAC AAC ACG GTC GTC GAT CGG TTC CGG CGG GTT TGG CTC TAC AGT GAG
JWTCR220	062	GAT CCC TCC TGG ACA CGC AGG ATG GAA GGA AGC TGC TCC ACC TGC TCA GCA CGA ACA ACA CGG TCG TCG ATC GGT TCC GGC GGG GC
JWTCR 219	063	CAT GGC CCC GCC GGA ACC GAT CGA CGA CCG TGT TGT TCG TGC TGA GCA GGT GGA GCA GCT TCC TTC CAT CCT GCG TGT CCA GGA GG

Fig. 21D

Primer	Seq Id No	Sequence (5' to 3')
JWTCR218	064	GAG GTG GAA TTC TAT TAA GAC TCC TTA TTA CGC AGT ATG
JWTCR217B	065	GAG GAG GTG GTG ACT AGT AGC AGG TTC TGG TGG GTT CTG GAT GTT TGG CTC TAC AGT GAG
JWTCR217	066	GAG GAG GTG GTG ACT AGA AGC AGG TTC TGG GTT CTG GAT GTT TGG CTC TAC AGT GAG
JWTCR216	067	GAG GTG GAA TTC TAT TAG TGA TGA TGG TGA TGG TGA GAC TCC TTA TTA CGC
JWTCR215	068	GAG GTG CCC GGG ACT GTT GAA AGT TGT TTA GC
JWTCR214	069	GAG GTG GAA TTC TAT TAG TGA TGA TGG TGA TGG TGG CTT GCT TTC GAG G
JWTCR213	070	GAG GTG GAA TTC TAT TAG CTT GCT TTC GAG G
JWTCR212	071	GAG GTG CCC GGG GCT GAG GGT GAC GAT CCC G
JWTCR211	072	AAT TCT CAT CAG TGA TGA TGG TGA TGG TGC
JWTCR210	073	CCG GGC ACC ATC ACC ATC ATC ACT GAT GAG
JWTCR209	074	GTG GAG CCC GGG TTC CAT CGG CAT GTA CTC TTC TTC CTC TAC AAC TGT GAG TCT GG
JWTCR208	075	GAG GTG GAA TTC TCA CCC GGG TTC CAT CGG CAT GTA CTC TTC TTC CTC GTC TGC TCG GCC CCA G
JWTCR207	076	GAG GTG CTG CAG GTT CCA TCG GCA TGT ACT CTT CTT CCT CGT CTA GAC GGC CCC AGG CCT C
JWTCR206	077	GTG GAG CTG CAG GGT CTA GAC GGC CCC AGG CCT C
JWTCR204	078	GTG GAG CTG CAG GTG ATC CAC CCC CTC CAG ATC CAC CCC CTC CGT CTG CTC GGC CCC AG
JWTCR202	079	GTG GAG AAG CTT TGC CGA GCA GGT GGA GCA GC

Fig. 21E

Primer	Seq Id No	Sequence (5' to 3')
JWTCR200A	080	GGG GGG GAG GTG CTC GAG CGA GGC AGC AGT CAC C
JWTCR23A	081	GAG CCC ACT AGT TTG GCT CTA CAG TGA GTT TGG TG
JWTCR1	082	CTA GAC CAG CAA ATC TGC ACC CAC AGA ATC CCT AGG ACA GCT CCC AGG TTC CTC TGC ATG GTG GA
JWTCR2	083	AGC TTC CAC CAT GCA GAG GAA CCT GGG AGC TGT CCT AGG GAT TCT GTG GGT GCA GAT TTG CTG GT
JWTCR3	084	GAT CGG TCT AGA GGT GAG CAG GTG GAG CAG CTT CC
JWTCR4	085	GCC TGG AGA CTC AGC CAT G
JWTCR5	086	GAA GTA CAT GGC TGA GTC TCC
JWTCR6	087	GAT GAA CGT TCC AGA TTC CAT GG
JWTCR7	088	CCC AAA TCA ATG TGC CGA AAA C
JWTCR8	089	CTA GAA CAC AGG AGA CTG GAG AGC ACG AAG AAG AGC CTG GAG CCC ATG GTG GA
JWTCR9	090	GCT CTC CTT GTA GGC CTG AG
JWTCR10	091	GTA CTT CTG TGC CAG CGG TG
JWTCR11	092	GAG CAA TTA TAG CTA CTG CCT G
JWTCR12	093	GGT CTG GAG GCC TTG TAT CC
JWTCR13	094	AGC TTC CAC CAT GGG CTC CAG GCT CTT CTT CGT GCT CTC CAG TCT CCT GTG TT
JA301	095	TCG AGG AAC CGC CAC CGC CAG AAC CGC CGC CAC CGG AAC CAC CAC CGC CGC TGC CAC CGC CAC CA

Fig. 21F

Primer	Seq. Id No.	
JA302	96	CTA GTG GTG GCG GTG GCA GCG GCG GTG GTC GTT CCG GTG GCG GCG GTT CTG GCG GTG GCC GTT CC
Kozak consensus	97	CCACCATG
	98	Glu Glu Glu Glu Tyr Met Pro Met Glu 1 5
	99	ATG AAA TAC CTG CTG CCG ACC GCA GCT GCT GGT CTG CTG CTG GCT GGC GGC CCA AGC CGT TGG CC
	100	MKY LLP TAA AAL LLL AAQ PAM

Fig. 21G

Seq. Id. No.	TCR-Vc Primers:	
116	5'-	Vc1&4
117	5'-	12,5
118	5'-	1,15
119	5'-	9
120	5'-	13,14
121	5'-	17
122	5'-	8
123	5'-	2,16
124	5'-	10
125	5'-	3,5
126	5'-	7
127	5'-	11

TCR-Vc BACK:

128	5'- SpeI	

129	5'-	-3'
130	3'-	-5'

Fig. 22

Seq. Id No.	TC2-7β SENT:	
101	5′-[redacted]	Vβ2,4
102	5′-[redacted]	10,14
103	5′-[redacted]	3
104	5′-[redacted]	11,9
105	5′-[redacted]	13,5-1
106	5′-[redacted]	15
107	5′-[redacted]	6
108	5′-[redacted]	8-3,12
109	5′-[redacted]	1
110	5′-[redacted]	8-1,2,4
111	5′-[redacted]	8-3,15
112	5′-[redacted]	15
113	5′-[redacted][a]	20

TC2-7β BACK:

Mixture of:

114	5′-[redacted]	
115	5′-[redacted]	

NcoI

[a]two colors were added, because full lenght vβ20 cDNA was not available.

Fig. 23